



SEQUENCE LISTING:

<110> Leong, Steven R.
Punnonen, Juha

<120> CYTOKINE POLYPEPTIDES AND NUCLEIC ACIDS

<130> 02-108010US

<150> 60/169,035

<151> 1999-12-02

<160> 44

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<211> 975

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Sequence

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gagtataaga agtacagagt ggagtgtcag gagggcagtg cctgcccagc cgctgaggag 600
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agcagcttct tcactcagaga catcatcaaa ccagaccac ccaagaacct gcaactgaag 720
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ccacattcct acttctccct gacattctgc atccagggtc agggcaagag caagagagaa 840
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gcccctggag aaatggtggt cctgcgctgt gacactcctg aagaagatgg catcacctgg 180
acctcagacc agagcagtga ggtcttgggc actggcaaaa ccctgaccat ccacgtcaaa 240
gagtttggag atgctggcca gtacacctgt cgcaaaggag gcgcagttct gagccagtca 300
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. aaagagccca aaâacaagag ctttctaaaa tgtgaggcaa agaattactc cggacgttttc 420
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ggctcctctg acccccagag ggtgacgtgc ggagcagcgt tgcctctcagc agagaaggtc 540
agcttggagc atagggagta taagaagtac agagtggagt gtcaggaggg cagtgcctgc 600
ccagccgctg aggagagcct gccattgag gtcgtgctgg aagctgttca caagctcaag 660
tatgaaaact ataccagcag cttcttcac agggacatca tcaaaccgga cccacccaag 720
aacctgcaac tgagaccact aaagaattct cggcaggtgg aggtcaactg ggagtaccct 780
gacacgtgga gcaccccaca ttctacttc tccctgacgt tttgtgttca ggtccaggga 840
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<210> 3

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Sequence

<400> 3

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acctcagacc agagcagtg ggtcttgggc actggcaaaa ccctgaccat ccacgtcaaa 240
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aaagaaccca aagctaagag ttttttaaaa tgtgaggcaa aggattattc tggacacttc 420
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ggctcctctg accccaag ggtgacttgt ggagccgtta cactctctgc agagagggtc 540
agcatggacc acagggagta taacaagtac acagtggagt gtcaggaggg cagtgcctgc 600
ccctctgccg aggagagcct acccatcgag gtcgtggtgg atgctattca caagctcaag 660
tatgaaaact acaccagcag cttcttcac agggacatca tcaaaccgga cccacccaag 720
aacttgacgc tgagaccact aaagaattct cggcaggtgg aggtcaactg ggagtaccct 780
gacacgtgga gcaccccaca ttctacttt tccctgacgt tttgtgttca ggtccaggga 840
aagaacaaga gagaaaagaa actcttcacg gaccaaactc cagccaaagt cacatgccac 900
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984

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<210> 4

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Sequence

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gtcctggag aaacagtggt cctcgctgt gacactcctg aagaagatgg catcacctgg 180
acctcagacc agagcagtga ggtcctgggc actggcaaaa ccctgaccat ccacgtcaaa 240
gagtttggag atgctggcca gtacacctgt cgcaaaggag gcgcagttct gagccagtca 300
ctcctgctgc ttcacaaaaa ggaagatgga atttgggtcca ctgatatttt aaagaccag 360
aaaaagccca aaaacaagat ctttctgaaa tgtgaggcaa agaattactc cggacgtttc 420
acctgctggt ggctgacagc aatcagtaca gatttgaaat tcaactgtcaa aagcagcaga 480
ggctcctctg accccaag ggtgacttgt ggagccgtta cactctctgc agagagggtc 540
agcatggacc acagggagta taacaagtac acagtggagt gtcaagaggg cagtgcctgc 600
ccctctgccg aggagagcct acccatcgag gtcgtggtgg atgctattca caagctcaag 660
tatgaaaact acaccagcag gttcttcac agggacatca tcaaaccgga cccacccaag 720

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aacttgcaac	tgagaccact	aaagaattct	cgacacgtgg	agatcagctg	ggagtaccct	780
gacacctgga	gcacccaca	ttcctacttc	tccctgacgt	tttgtgttca	ggtccagggg	840
aagaacaaga	gagaaaagaa	actcttcatg	gaccaaacct	cagccaaagt	cacatgccac	900
aaggatgcca	agatccgctg	gcaagccaga	gaccgctacc	acagctcatc	ttggagcgaa	960
tgggcatctg	tgccctgcag	ttag				984

<210> 5

<211> 969

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Sequence

<400> 5

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gcccctggag	aaatggtggt	cctcgctgt	gacactcctg	aagaagatgg	catcacctgg	180
acctcagacc	agagcagtga	ggtcttgggc	actggcaaaa	ccctgaccat	ccacgtcaaa	240
gagtttggag	atgctggcca	gtatacctgc	cataaaggag	gcaaggttct	gagccgctca	300
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aaagagccca	aaaacaagag	ctttctaaaa	tgtgaggcaa	agaattactc	cggacgtttc	420
acctgctggt	ggctgacgac	aatcagttact	gatctgacat	tcagtgtcaa	aagcagcaga	480
ggctctactg	acccccatgg	cgtgacatgt	ggcacggcaa	cgctctcaga	ggacctcgga	540
gagtataaga	agtacagagt	ggagtgtcag	gagggcagtg	cctgcccagc	cgctgaggag	600
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ccattaaaga	attctcggca	ggtggaggtc	aactgggagt	accctgacac	gtggagcacc	780
ccacattcct	actttctcct	gacgttttgg	gttcagggtcc	aggggaaggaa	caagagagaa	840
aagaaactct	tcattggacca	aacctcagcc	aaagtacagt	gccacaagga	tgccaagatc	900
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<210> 6

<211> 975

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Sequence

<400> 6

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gcccctggag	aaatggtggt	cctcgctgt	gacactcctg	aagaagatgg	catcacctgg	180
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gagtttggag	atgctggcca	gtacacctgt	cataaaggag	gcacagttct	gagccagtca	300
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gatagactct	tcattggacca	aacctcagcc	aaagtctgtg	gccacaagga	tgccaagatc	900
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<213> Artificial Sequence

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gcccctggag aaatggtggt cctcgctgtg gacactcctg aagaagatgg catcacctgg 180
acctcagacc agagcagtga ggtcttgggc actggcaaaa ccctgaccat ccacgtcaaa 240
gagtttggag atgctggcca gtacacctgt cgcaaaggag gcgcagttct gagccagtca 300
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ccctctgccg aggagagcct acccatcgag gtcgtggtgg atgctattca caagctcaag 660
tatgaaaact acaccagcag cttcttcatc agagacatca tcaaacctga cccacccaag 720
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<210> 8
<211> 324
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 8
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Ala Ser Pro Leu Met Ala Ile Trp Glu Leu Lys Lys Asp Val Tyr Val
20 25 30
Val Glu Leu Asp Trp Tyr Pro Asn Ala Pro Gly Glu Thr Val Val Leu
35 40 45
Thr Cys Asp Thr Pro Glu Glu Asp Gly Ile Thr Trp Thr Ser Asp Gln
50 55 60
Ser Ser Glu Val Leu Gly Thr Gly Lys Thr Leu Thr Ile His Val Lys
65 70 75 80
Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys Arg Lys Gly Gly Glu Ala
85 90 95
Leu Ser Arg Ser Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp
100 105 110
Ser Thr Asp Ile Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Ser Phe
115 120 125
Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
130 135 140
Leu Thr Thr Ile Ser Thr Asp Leu Lys Phe Ser Val Lys Ser Ser Arg
145 150 155 160
Gly Ser Thr Asp Pro Arg Gly Val Thr Cys Gly Thr Ala Thr Leu Ser
165 170 175
Glu Asp Leu Gly Glu Tyr Lys Lys Tyr Arg Val Glu Cys Gln Glu Gly
180 185 190
Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Val Leu

		195					200					205					
Glu	Ala	Val	His	Lys	Leu	Lys	Tyr	Glu	Asn	Tyr	Thr	Ser	Ser	Phe	Phe		
	210						215					220					
Ile	Arg	Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Lys	Asn	Leu	Gln	Leu	Lys		
225					230					235					240		
Pro	Leu	Lys	Asn	Ser	Arg	His	Val	Glu	Val	Ser	Trp	Gly	Tyr	Pro	Asp		
			245						250					255			
Thr	Trp	Ser	Thr	Pro	His	Ser	Tyr	Phe	Ser	Leu	Thr	Phe	Cys	Ile	Gln		
			260					265					270				
Val	Gln	Gly	Lys	Ser	Lys	Arg	Glu	Lys	Lys	Asp	Arg	Ile	Phe	Thr	Asp		
		275					280					285					
Lys	Thr	Ser	Ala	Thr	Val	Ile	Cys	Arg	Lys	Asn	Ala	Lys	Ile	Arg	Val		
	290					295					300						
Gln	Ala	Arg	Asp	Arg	Tyr	Tyr	Ser	Ser	Phe	Trp	Ser	Glu	Trp	Ala	Ser		
305					310					315					320		
Val	Ser	Cys	Ser														

<210> 9
 <211> 327
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Sequence

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			20					25				30					
Val	Glu	Leu	Asp	Trp	Tyr	Pro	Asp	Ala	Pro	Gly	Glu	Met	Val	Val	Leu		
		35					40					45					
Ala	Cys	Asp	Thr	Pro	Glu	Glu	Asp	Gly	Ile	Thr	Trp	Thr	Ser	Asp	Gln		
	50					55					60						
Ser	Ser	Glu	Val	Leu	Gly	Thr	Gly	Lys	Thr	Leu	Thr	Ile	His	Val	Lys		
65					70					75					80		
Glu	Phe	Gly	Asp	Ala	Gly	Gln	Tyr	Thr	Cys	Arg	Lys	Gly	Gly	Ala	Val		
			85						90					95			
Leu	Ser	Gln	Ser	Leu	Leu	Leu	Leu	His	Lys	Lys	Glu	Asp	Gly	Ile	Trp		
			100					105					110				
Ser	Thr	Asp	Ile	Leu	Lys	Asp	Gln	Lys	Glu	Pro	Lys	Asn	Lys	Ser	Phe		
	115					120						125					
Leu	Lys	Cys	Glu	Ala	Lys	Asn	Tyr	Ser	Gly	Arg	Phe	Thr	Cys	Trp	Trp		
	130					135					140						
Leu	Thr	Thr	Ile	Ser	Thr	Asp	Leu	Lys	Phe	Ser	Val	Lys	Ser	Ser	Arg		
145					150					155					160		
Gly	Ser	Ser	Asp	Pro	Arg	Gly	Val	Thr	Cys	Gly	Ala	Ala	Leu	Leu	Ser		
			165						170						175		
Ala	Glu	Lys	Val	Ser	Leu	Glu	His	Arg	Glu	Tyr	Lys	Lys	Tyr	Arg	Val		
			180					185					190				
Glu	Cys	Gln	Glu	Gly	Ser	Ala	Cys	Pro	Ala	Ala	Glu	Glu	Ser	Leu	Pro		
	195						200					205					
Ile	Glu	Val	Val	Leu	Glu	Ala	Val	His	Lys	Leu	Lys	Tyr	Glu	Asn	Tyr		
	210					215						220					
Thr	Ser	Ser	Phe	Phe	Ile	Arg	Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Lys		
225					230					235					240		
Asn	Leu	Gln	Leu	Arg	Pro	Leu	Lys	Asn	Ser	Arg	Gln	Val	Glu	Val	Asn		
			245						250					255			
Trp	Glu	Tyr	Pro	Asp	Thr	Trp	Ser	Thr	Pro	His	Ser	Tyr	Phe	Ser	Leu		

<210> 11
 <211> 327
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Sequence

<400> 11
 Met His Pro Gln Gln Leu Val Val Ser Trp Phe Ser Leu Val Leu Leu
 1 5 10 15
 Ala Ser Pro Leu Val Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val
 20 25 30
 Val Glu Leu Asp Trp Tyr Pro Asp Ala Pro Gly Glu Thr Val Val Leu
 35 40 45
 Ala Cys Asp Thr Pro Glu Glu Asp Gly Ile Thr Trp Thr Ser Asp Gln
 50 55 60
 Ser Ser Glu Val Leu Gly Thr Gly Lys Thr Leu Thr Ile His Val Lys
 65 70 75 80
 Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys Arg Lys Gly Gly Ala Val
 85 90 95
 Leu Ser Gln Ser Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp
 100 105 110
 Ser Thr Asp Ile Leu Lys Asp Gln Lys Lys Pro Lys Asn Lys Ile Phe
 115 120 125
 Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
 130 135 140
 Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg
 145 150 155 160
 Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Val Thr Leu Ser
 165 170 175
 Ala Glu Arg Val Ser Met Asp His Arg Glu Tyr Asn Lys Tyr Thr Val
 180 185 190
 Glu Cys Gln Glu Gly Ser Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro
 195 200 205
 Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr
 210 215 220
 Thr Ser Arg Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys
 225 230 235 240
 Asn Leu Gln Leu Arg Pro Leu Lys Asn Ser Arg His Val Glu Ile Ser
 245 250 255
 Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
 260 265 270
 Thr Phe Cys Val Gln Val Gln Gly Lys Asn Lys Arg Glu Lys Lys Leu
 275 280 285
 Phe Met Asp Gln Thr Ser Ala Lys Val Thr Cys His Lys Asp Ala Lys
 290 295 300
 Ile Arg Val Gln Ala Arg Asp Arg Tyr His Ser Ser Ser Trp Ser Glu
 305 310 315 320
 Trp Ala Ser Val Pro Cys Ser
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<210> 12
 <211> 322
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic Sequence

<400> 12

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Met Cys His Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Phe Leu
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Ala Ser Pro Leu Val Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val
          20          25          30
Val Glu Leu Asp Trp Tyr Pro Asp Ala Pro Gly Glu Met Val Val Leu
          35          40          45
Ala Cys Asp Thr Pro Glu Glu Asp Gly Ile Thr Trp Thr Ser Asp Gln
          50          55          60
Ser Ser Glu Val Leu Gly Thr Gly Lys Thr Leu Thr Ile His Val Lys
65          70          75          80
Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Lys Val
          85          90          95
Leu Ser Arg Ser Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp
          100          105          110
Ser Thr Asp Ile Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Ser Phe
          115          120          125
Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
          130          135          140
Leu Thr Thr Ile Ser Thr Asp Leu Thr Phe Ser Val Lys Ser Ser Arg
145          150          155          160
Gly Ser Thr Asp Pro His Gly Val Thr Cys Gly Thr Ala Thr Leu Ser
          165          170          175
Glu Asp Leu Gly Glu Tyr Lys Lys Tyr Arg Val Glu Cys Gln Glu Gly
          180          185          190
Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Val Leu
          195          200          205
Glu Ala Val His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe
          210          215          220
Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Arg
225          230          235          240
Pro Leu Lys Asn Ser Arg Gln Val Glu Val Asn Trp Glu Tyr Pro Asp
          245          250          255
Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Val Gln
          260          265          270
Val Gln Gly Arg Asn Lys Arg Glu Lys Lys Leu Phe Met Asp Gln Thr
          275          280          285
Ser Ala Lys Val Thr Cys His Lys Asp Ala Lys Ile Arg Val Gln Ala
          290          295          300
Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asp Trp Ala Ser Val Ser
305          310          315          320
Cys Gly

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<210> 13

<211> 324

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Sequence

<400> 13

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Met Cys His Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Phe Leu
 1          5          10          15
Ala Ser Pro Leu Met Ala Ile Trp Glu Leu Lys Lys Asp Val Tyr Val
          20          25          30
Val Glu Leu Asp Trp Tyr Pro Asp Ala Pro Gly Glu Met Val Val Leu

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			100					105				110				
Ser	Thr	Asp	Ile	Leu	Lys	Asp	Gln	Lys	Glu	Pro	Lys	Asn	Lys	Ile	Phe	
		115					120					125				
Leu	Lys	Cys	Glu	Ala	Lys	Asn	Tyr	Ser	Gly	Arg	Phe	Thr	Cys	Trp	Trp	
	130					135					140					
Leu	Thr	Ala	Ile	Ser	Thr	Asp	Leu	Lys	Phe	Thr	Val	Lys	Ser	Ser	Arg	
145					150					155					160	
Gly	Ser	Ser	Asp	Pro	Gln	Gly	Val	Thr	Cys	Gly	Ala	Val	Thr	Leu	Ser	
			165						170					175		
Ala	Glu	Arg	Val	Ser	Met	Asp	His	Arg	Glu	Tyr	Asn	Lys	Tyr	Thr	Val	
			180					185					190			
Glu	Cys	Gln	Glu	Gly	Ser	Ala	Cys	Pro	Ser	Ala	Glu	Glu	Ser	Leu	Pro	
	195						200					205				
Ile	Glu	Val	Val	Val	Asp	Ala	Ile	His	Lys	Leu	Lys	Tyr	Glu	Asn	Tyr	
	210					215						220				
Thr	Ser	Ser	Phe	Phe	Ile	Arg	Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Lys	
225					230					235					240	
Asn	Leu	Gln	Leu	Lys	Pro	Leu	Lys	Asn	Ser	Arg	His	Val	Glu	Ile	Ser	
			245					250					255			
Trp	Glu	Tyr	Pro	Asp	Thr	Trp	Ser	Ile	Pro	His	Ser	Tyr	Phe	Ser	Leu	
		260						265					270			
Met	Phe	Gly	Val	Gln	Val	Gln	Gly	Lys	Asn	Lys	Arg	Glu	Lys	Lys	Asp	
	275						280					285				
Arg	Leu	Ser	Val	Asp	Lys	Thr	Ser	Ala	Lys	Val	Val	Cys	His	Lys	Asp	
	290					295					300					
Ala	Lys	Ile	Arg	Val	Gln	Ala	Arg	Asp	Arg	Tyr	Tyr	Ser	Ser	Ser	Trp	
305					310				315						320	
Ser	Glu	Trp	Ala	Ser	Val	Pro	Cys	Ser								
			325													

<210> 15
 <211> 328
 <212> PRT
 <213> Homo sapiens

<400> 15

Met	Cys	His	Gln	Gln	Leu	Val	Ile	Ser	Trp	Phe	Ser	Leu	Val	Phe	Leu	
1				5					10					15		
Ala	Ser	Pro	Leu	Val	Ala	Ile	Trp	Glu	Leu	Lys	Lys	Asp	Val	Tyr	Val	
			20					25					30			
Val	Glu	Leu	Asp	Trp	Tyr	Pro	Asp	Ala	Pro	Gly	Glu	Met	Val	Val	Leu	
	35						40					45				
Thr	Cys	Asp	Thr	Pro	Glu	Glu	Asp	Gly	Ile	Thr	Trp	Thr	Leu	Asp	Gln	
	50					55					60					
Ser	Ser	Glu	Val	Leu	Gly	Ser	Gly	Lys	Thr	Leu	Thr	Ile	Gln	Val	Lys	
65					70				75						80	
Glu	Phe	Gly	Asp	Ala	Gly	Gln	Tyr	Thr	Cys	His	Lys	Gly	Gly	Glu	Val	
			85					90					95			
Leu	Ser	His	Ser	Leu	Leu	Leu	Leu	His	Lys	Lys	Glu	Asp	Gly	Ile	Trp	
			100					105					110			
Ser	Thr	Asp	Ile	Leu	Lys	Asp	Gln	Lys	Glu	Pro	Lys	Asn	Lys	Thr	Phe	
	115						120					125				
Leu	Arg	Cys	Glu	Ala	Lys	Asn	Tyr	Ser	Gly	Arg	Phe	Thr	Cys	Trp	Trp	
	130					135					140					
Leu	Thr	Thr	Ile	Ser	Thr	Asp	Leu	Thr	Phe	Ser	Val	Lys	Ser	Ser	Arg	
145					150				155						160	
Gly	Ser	Ser	Asp	Pro	Gln	Gly	Val	Thr	Cys	Gly	Ala	Ala	Thr	Leu	Ser	
			165					170					175			
Ala	Glu	Arg	Val	Arg	Gly	Asp	Asn	Lys	Glu	Tyr	Glu	Tyr	Ser	Val	Glu	
			180					185					190			

Cys	Gln	Glu	Asp	Ser	Ala	Cys	Pro	Ala	Ala	Glu	Glu	Ser	Leu	Pro	Ile
		195					200					205			
Glu	Val	Met	Val	Asp	Ala	Val	His	Lys	Leu	Lys	Tyr	Glu	Asn	Tyr	Thr
		210					215				220				
Ser	Ser	Phe	Phe	Ile	Arg	Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Lys	Asn
225					230					235					240
Leu	Gln	Leu	Lys	Pro	Leu	Lys	Asn	Ser	Arg	Gln	Val	Glu	Val	Ser	Trp
				245					250						255
Glu	Tyr	Pro	Asp	Thr	Trp	Ser	Thr	Pro	His	Ser	Tyr	Phe	Ser	Leu	Thr
			260					265					270		
Phe	Cys	Val	Gln	Val	Gln	Gly	Lys	Ser	Lys	Arg	Glu	Lys	Lys	Asp	Arg
		275					280					285			
Val	Phe	Thr	Asp	Lys	Thr	Ser	Ala	Thr	Val	Ile	Cys	Arg	Lys	Asn	Ala
		290					295				300				
Ser	Ile	Ser	Val	Arg	Ala	Gln	Asp	Arg	Tyr	Tyr	Ser	Ser	Ser	Trp	Ser
305					310					315					320
Glu	Trp	Ala	Ser	Val	Pro	Cys	Ser								
					325										

<210> 16
 <211> 666
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Sequence

<400> 16
 atgtgcccac ttcgcagcct cctcctcata tccaccctgg ttctcctcca ccacctgccc 60
 cacctcagtt tgggcaggag cctccccacc accacagcaa gcccaggaag gagctgcctc 120
 gactactccc aaaacctgtt gaaggccgcc agcaacacgc ttcagaaggc cagacaaatt 180
 ctagaatttt acccttgcac ttctgaggag atcgatcatg aagatatcac caaagataaa 240
 accagcacag tggaggcctg tttaccactg gaattagcca cgaatgagag ttgcctggct 300
 tccagagaga tctctctgat aactaatggg agttgcctgg cttccagaaa gacctctttt 360
 atgacaaccc tgtgccatag cagcatctat gaggacttga agatgtacca gatggaattc 420
 aaggccatga acgcaaagct tttgatggat cctaagaggc agatctttct agatcaaaac 480
 atgctggcag ttattgatga gctgatgcag gccctgaatt tcaacagtga gactgtgcc 540
 cagaagccct ccctggaaga actggatttt tataagacta aaatcaagct ctgcatactt 600
 cttcatgcct tcagaattcg tgcggtgacc atcgacagaa tgatgagcta tctgaattct 660
 tcctaa 666

<210> 17
 <211> 666
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Sequence

<400> 17
 atgtacccac ttcgcagcct cctcctcata tccaccctgg ttctcctcca ccacctgccc 60
 cacctcagtt tgggcaggag cctccccacc accacagcaa gcccaggaag gagctgcctc 120
 gactactccc aaaacctgtt gaaggccgcc agcaacacgc ttcagaaggc cagacaaatt 180
 ctagaatttt acccttgcac ttctgaggag atcgatcatg aagatatcac caaagataaa 240
 accagcacag tggaggcctg tttaccactg gaattagcca cgaatgagag ttgcctggct 300
 tccagagaga tctctctgat aactaatggg agttgcctgg cttccagaaa gacctctttt 360
 atgacaaccc tgtgccttag cagcatctat gaggacttga agatgtacca gatggaattc 420
 aaggccatga acgcaaagct tttgatggat cctaagaggc agatcttttt agatcaaaac 480
 atgctggcag ttattgatga gctgatgcag gccctgaatt tcaacagtga gactgtgcc 540
 cagaagccct ccctggaaga actggatttt tataagacta aaatcaagct ctgcatactt 600

cttcatgcct tcagaattcg ggcagtgacc atcaatagaa tgatgagcta tctgaattct 660
tcctag 666

<210> 18

<211> 660

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Sequence

<400> 18

atgtgcccgc cgcgcgccct cctccttggt gctaccctgg tctcctgga ccacctcagt 60
ttggccagaa acctccctgt ggccacccca ggcccaggaa tgttcccatg ccttcaccac 120
tcccaaaacc tgctgagggc cgtcagcaac atgctgcaga aggccagaca aactctagaa 180
ttttactcct gcacttccga agagattgat catgaagata tcacaaaaga taaaaccagc 240
acagtggagg cctgcttacc actggaatta atcaagaatg agagttgcct aaattccaga 300
gagacttctt tcataactaa tgggagttgc ctaccctcca gaaagacctc ttttatgaca 360
accctgtgcc ttagcagtat ctatgaggac ttgaagatgt accaggtgga gttcaagacc 420
atgaatgcaa agcttctgat gaatcctaag aggcagatct ttctggatca aaacatgctg 480
acagctattg atgagctgtt acaggccctg aatttcaaca gtgagactgt gccacaaaaa 540
tctcctcttg aagaaccgga tttttataaa actaaaatca agctctgcat acttcttcat 600
gctttcagaa ttcgggcagt gaccatcaat agaatgatga gctatctgaa ttcttcctag 660

<210> 19

<211> 660

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Sequence

<400> 19

atgtgtccag cgcgcagcct cctccttggt gctaccctgg tctcctgga ccacctcagt 60
ttggccagaa acctccctgt ggccacccca ggcccaggaa tgttcccatg ccttcaccac 120
tcccaaaacc tgctgagggc tgtcagcaac acgctccaga aggccaaaca aaccctagaa 180
ttttaccctt gcacttccga agagattgat catgaagata tcacacaaga taaaaccagc 240
acagtggagg cctgtttacc actggaatta gccacgaatg agagttgcct ggcttccaga 300
gggatctctc tgataactaa tgggagttgc ctggcctcca gaaagacctc ttttatgacg 360
accctgtgcc ttagcagtat ctatgaggac ttgaagatgt accaggtgga gttcaaggcc 420
atgaatgcaa agctgttaat ggatcctaaa aggcagatct ttctggatca aaacatgctg 480
gcagctattg ctgagctaat gcaggccctg aatgtcaaca gtgagactgc gccacaaaaa 540
tctcctcttg aagaaccgga tttttataaa actaaaatca agctctgcat acttcttcat 600
gctttcagaa ttcgtgcagt gaccatcaat agaatgatga gctatctgaa ttcttcctag 660

<210> 20

<211> 660

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Sequence

<400> 20

atgtgtccag cgcgcagcct cctccttggt gctaccctgg tctcctgga ccacctcagt 60
ttggccagaa acctccctgt ggccacccca ggcccaggaa tgttcccatg ccttcaccac 120
tcccaaaacc tgctgagggc cgtcagcaac atgctgcaga aggccagaca aactctagaa 180
ttttactcct gcacttccga agagattgat catgaagata tcacaaaaga taaaaccagc 240
acagtggagg cctgcttacc actggaatta atcaagaatg agagttgcct aaattccaga 300

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.gagacttctt tcataactaa tgggagttgc ctagcctcca gaaagacctc ttttatgaca 360
accctgtgccc ttagcagtat ctatgaggac ttgaagatgt accaggtgga gttcaaggcc 420
atgaatgcaa agctgttaat ggatcctaaa aggcagatct ttctggatca aaacatgctg 480
gcagctattg ctgagctaata gcaggccctg aatgtcaaca gtgagactgc gccacaaaaa 540
tcctcccttg aagaaccgga tttttataaa actaaaatca agctctgcat acttcttcat 600
gctttcagaa ttcgtgcagt gaccatcaat agaatgatga gctatctgaa ttcttcctag 660

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<210> 21

<211> 660

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Sequence

<400> 21

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atgtgtccag cgcgagcct cctccttgtg gctaccctgg tcctcctgga ccacctcagt 60
ttggccagaa acctccccgt ggccactcca gaccagga tggtcccatg ccttcaccac 120
tccccaaaacc tgctgagggc cgtcagcaac atgctgcaga aggccagaca aactctagaa 180
ttttactcct gcacttccga agagattgat catgaagata tcacaaaaga taaaaccagc 240
acagtggagg cctgtttacc actggaatta gccacgaatg agagttgcct ggcttccaga 300
gggatctctc tgataactaa tgggagttgc ctagcctcca gaaagacctc ttttatgacg 360
accctgtgcc ttggcagtat ctatgaggac ttgaagatgt accaggtgga gttcaagacc 420
atgaatgcaa agcttctgat gaatcctaag aggcagatct ttctggatca aaacatgctg 480
acagctattg atgagctgtt acaggccctg aatttcaaca gtgagactgt gccacaaaaa 540
tcctcccttg aagaaccgga tttttataaa actaaaatca agctctgcat acttcttcat 600
gctttcagaa ttcgggcagt gaccatcaat agaatgatga gctatctgaa ttcttcctag 660

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<210> 22

<211> 660

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Sequence

<400> 22

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atgtgcccgc cgcgcggcct cctccttgtg gctaccctgg tcctcctgga ccacctcagt 60
ttggccagaa acctccctgt ggccacccca ggcccaggaa tggtcccatg ccttcaccac 120
tccccaaaacc tgctgagggc cgtcagcaac atgctgcaga aggccagaca aactctagaa 180
ttttactcct gcacttccga agagactgat catgaagata tcacaaaaga taaaaccagc 240
acagtggagg cctgcttacc actggaatta atcaagaatg agagttgcct aaattccaga 300
gagacttctt tcataactaa tgggagttgc ctagcctcca gaaagacctc ttttatgaca 360
accctgtgcc ttagcagtat ctatgaggac ttgaagatgt accaggtgga gttcaagacc 420
atgaatgcaa agcttctgat gaatcctaag aggcagatct ttctggatca aaacatgctg 480
acagctattg atgagctgtt acaggccctg aatttcaaca gtgagactgt gccacaaaaa 540
tcctcccttg aagaaccgga tttttataaa actaaaatca agctctgcat acttcttcat 600
gctttcagaa ttcgggcagt gaccatcaat agaatgatga gctatctgaa ttcttcctag 660

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<210> 23

<211> 660

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Sequence

<400> 23

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atgtgcccgc cgcgcgccct cctccttgtg gctaccctgg tcctcctgga ccacctcagt 60
ttggccagaa acctccccgt ggccacccca ggcccaggaa tggtcccatg ccttcaccac 120
tcccaaaacc tgctgagggc tgtcagcaac acgctccaga aggccaaaca aaccctagaa 180
ttttaccctt gcacttccga agagattgat catgaagata tcacaaaaga taaaaccagc 240
acagtggagg cctgtttacc actggaatta gccacgaatg agagttgcct ggcttccaga 300
gggatctctc tgataactaa tgggagttgc ctggcctcca gaaagacctc ttttatgaca 360
accctgtgcc ttagcagcat ctatgaggac ttgaagatgt accaggtgga gttcaaggcc 420
atgaatgcaa agctgttaat ggatcctaaa aggcagatct ttctggatca aaacatgctg 480
gcagctattg ctgagctaata gcaggccctg aatgtcaaca gtgagactgc gccacaaaaa 540
tcctccctgg aagaaccgga tttttataaa actaaaatca agctctgcat acttcttcat 600
gctttcagaa ttcgggcagt gaccatcaat agaatgatga gctatctgaa ttcttcctag 660

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<210> 24

<211> 660

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Sequence

<400> 24

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atgtgtccag cgcgcagcct cctccttgtg gctaccctgg tcctcctgga ccacctcagt 60
ttggccagaa acctccccgt ggccactcca gaccaggaa tggtcccatg ccttcaccac 120
tcccaaaacc tgctgagggc tgtcagcaac acgctccaga aggccaaaca aaccctagaa 180
ttttaccctt gcacttccga agagattgat catgaagata tcacaaaaga taaaaccagc 240
acagtggagg cctgtttacc actggaatta gccacgaatg agagttgcct ggcttccaga 300
gggatctctc tgataactaa tgggagttgc ctggcctcca gaaagacctc ttttatgacg 360
accctgtgcc ttagcagcat ctatgaggac ttgaagatgt accaggtgga gttcaaggcc 420
atgaatgcaa agctgttgat ggatcctaaa aggcagatct ttctggatca aaacatgctg 480
gcagctattg ctgagctaata gcaggccctg aatgtcaaca gtgagactgc gccacaaaaa 540
tcctcccttg aagaaccgga tttttataag actaaaatca agctctgcat acttcttcat 600
gccttcagaa ttcgtgcagt gaccatcgat agaatgatga gctatctgaa ttcttcctag 660

```

<210> 25

<211> 660

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Sequence

<400> 25

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atgtgcccgc cgcgcgccct cctccttgtg gctaccctgg tcctcctgga ccacctcagt 60
ttggccagaa acctccctgt ggccacccca ggcccaggaa tggtcccatg ccttcaccac 120
tcccaaaacc tgctgagggc cgtcagcaac atgctgcaga aggccagaca aactctagaa 180
ttttactcct gcacttccga agagattgat catgaagata tcacaaaaga taaaaccagc 240
acagtggagg cctgtttacc actggaatta atcaagaatg agagttgcct aaattccaga 300
gagacttctt tcataactaa tgggagttgc ctagcctcca gaaagacctc ttttatgaca 360
accctgtgcc ttagcagtat ctatgaggac ttgaagatgt accaggtgga gttcaagacc 420
atgaatgcaa agcttctgat gaatcctaag aggcagatct ttctggatca aaacatgctg 480
acagctattg atgagctgtt acaggccctg aatttcaaca gtgagactgt gccacaaaaa 540
tcctcccttg aagaaccgga tttttataaa actaaaatca agctctgcat acttcttcat 600
gctttcagaa ttcgggcagt gaccatcaat agaatgatga gctatctgaa ttcttcctag 660

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<210> 26

<211> 221

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Sequence

<400> 26

Met	Cys	Pro	Leu	Arg	Ser	Leu	Leu	Leu	Ile	Ser	Thr	Leu	Val	Leu	Leu
1				5					10					15	
His	His	Leu	Pro	His	Leu	Ser	Leu	Gly	Arg	Ser	Leu	Pro	Thr	Thr	Thr
			20					25					30		
Ala	Ser	Pro	Gly	Arg	Ser	Cys	Leu	Asp	Tyr	Ser	Gln	Asn	Leu	Leu	Lys
		35					40					45			
Ala	Ala	Ser	Asn	Thr	Leu	Gln	Lys	Ala	Arg	Gln	Ile	Leu	Glu	Phe	Tyr
	50					55					60				
Pro	Cys	Thr	Ser	Glu	Glu	Ile	Asp	His	Glu	Asp	Ile	Thr	Lys	Asp	Lys
65					70					75				80	
Thr	Ser	Thr	Val	Glu	Ala	Cys	Leu	Pro	Leu	Glu	Leu	Ala	Thr	Asn	Glu
				85					90					95	
Ser	Cys	Leu	Ala	Ser	Arg	Glu	Ile	Ser	Leu	Ile	Thr	Asn	Gly	Ser	Cys
			100						105				110		
Leu	Ala	Ser	Arg	Lys	Thr	Ser	Phe	Met	Thr	Thr	Leu	Cys	His	Ser	Ser
		115					120					125			
Ile	Tyr	Glu	Asp	Leu	Lys	Met	Tyr	Gln	Met	Glu	Phe	Lys	Ala	Met	Asn
	130					135					140				
Ala	Lys	Leu	Leu	Met	Asp	Pro	Lys	Arg	Gln	Ile	Phe	Leu	Asp	Gln	Asn
145					150					155				160	
Met	Leu	Ala	Val	Ile	Asp	Glu	Leu	Met	Gln	Ala	Leu	Asn	Phe	Asn	Ser
				165					170					175	
Glu	Thr	Val	Pro	Gln	Lys	Pro	Ser	Leu	Glu	Glu	Leu	Asp	Phe	Tyr	Lys
			180					185					190		
Thr	Lys	Ile	Lys	Leu	Cys	Ile	Leu	Leu	His	Ala	Phe	Arg	Ile	Arg	Ala
		195					200					205			
Val	Thr	Ile	Asp	Arg	Met	Met	Ser	Tyr	Leu	Asn	Ser	Ser			
	210					215						220			

<210> 27

<211> 221

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Sequence

<400> 27

Met	Tyr	Pro	Leu	Arg	Ser	Leu	Leu	Leu	Ile	Ser	Thr	Leu	Val	Leu	Leu
1				5					10					15	
His	His	Leu	Pro	His	Leu	Ser	Leu	Gly	Arg	Ser	Leu	Pro	Thr	Thr	Thr
			20					25					30		
Ala	Ser	Pro	Gly	Arg	Ser	Cys	Leu	Asp	Tyr	Ser	Gln	Asn	Leu	Leu	Lys
		35					40					45			
Ala	Ala	Ser	Asn	Thr	Leu	Gln	Arg	Ala	Arg	Gln	Ile	Leu	Glu	Phe	Tyr
	50					55					60				
Pro	Cys	Thr	Ser	Glu	Glu	Ile	Asp	His	Glu	Asp	Ile	Thr	Lys	Asp	Lys
65					70					75				80	
Thr	Ser	Thr	Val	Glu	Ala	Cys	Leu	Pro	Leu	Glu	Leu	Ala	Thr	Asn	Glu
				85					90					95	
Ser	Cys	Leu	Ala	Ser	Arg	Glu	Ile	Ser	Leu	Ile	Thr	Asn	Gly	Ser	Cys
			100						105				110		
Leu	Ala	Ser	Arg	Lys	Thr	Ser	Phe	Met	Thr	Thr	Leu	Cys	Leu	Ser	Ser
		115					120					125			
Ile	Tyr	Glu	Asp	Leu	Lys	Met	Tyr	Gln	Met	Glu	Phe	Lys	Ala	Met	Asn

130		135		140
Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn				
145		150		155
Met Leu Ala Val Ile Asp Glu Leu Met Gln Ala Leu Asn Phe Asn Ser				160
	165		170	
Glu Thr Val Pro Gln Lys Pro Ser Leu Glu Glu Leu Asp Phe Tyr Lys				175
	180		185	
Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala				190
	195		200	
Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ser Ser				205
	210		215	
				220

<210> 28
 <211> 219
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Sequence

<400> 28
Met Cys Pro Pro Arg Gly Leu Leu Leu Val Ala Thr Leu Val Leu Leu
1 5 10 15
Asp His Leu Ser Leu Ala Arg Asn Leu Pro Val Ala Thr Pro Gly Pro
20 25 30
Gly Met Phe Pro Cys Leu His His Ser Gln Asn Leu Leu Arg Ala Val
35 40 45
Ser Asn Met Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys
50 55 60
Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser
65 70 75 80
Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Ile Lys Asn Glu Ser Cys
85 90 95
Leu Asn Ser Arg Glu Thr Ser Phe Ile Thr Asn Gly Ser Cys Leu Ala
100 105 110
Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr
115 120 125
Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Thr Met Asn Ala Lys
130 135 140
Leu Leu Met Asn Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu
145 150 155 160
Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe Asn Ser Glu Thr
165 170 175
Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys
180 185 190
Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val Thr
195 200 205
Ile Asn Arg Met Met Ser Tyr Leu Asn Ser Ser
210 215

<210> 29
 <211> 219
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Sequence

<400> 29

Met	Cys	Pro	Ala	Arg	Ser	Leu	Leu	Leu	Val	Ala	Thr	Leu	Val	Leu	Leu
1				5					10					15	
Asp	His	Leu	Ser	Leu	Ala	Arg	Asn	Leu	Pro	Val	Ala	Thr	Pro	Gly	Pro
		20						25					30		
Gly	Met	Leu	Pro	Cys	Leu	His	His	Ser	Gln	Asn	Leu	Leu	Arg	Ala	Val
		35					40					45			
Ser	Asn	Thr	Leu	Gln	Lys	Ala	Lys	Gln	Thr	Leu	Glu	Phe	Tyr	Pro	Cys
	50					55					60				
Thr	Ser	Glu	Glu	Ile	Asp	His	Glu	Asp	Ile	Thr	Gln	Asp	Lys	Thr	Ser
65					70					75					80
Thr	Val	Glu	Ala	Cys	Leu	Pro	Leu	Glu	Leu	Ala	Thr	Asn	Glu	Ser	Cys
				85					90					95	
Leu	Ala	Ser	Arg	Gly	Ile	Ser	Leu	Ile	Thr	Asn	Gly	Ser	Cys	Leu	Ala
			100					105					110		
Ser	Arg	Lys	Thr	Ser	Phe	Met	Thr	Thr	Leu	Cys	Leu	Ser	Ser	Ile	Tyr
	115						120					125			
Glu	Asp	Leu	Lys	Met	Tyr	Gln	Val	Glu	Phe	Lys	Ala	Met	Asn	Ala	Lys
	130					135					140				
Leu	Leu	Met	Asp	Pro	Lys	Arg	Gln	Ile	Phe	Leu	Asp	Gln	Asn	Met	Leu
145					150					155					160
Ala	Ala	Ile	Ala	Glu	Leu	Met	Gln	Ala	Leu	Asn	Val	Asn	Ser	Glu	Thr
				165					170					175	
Ala	Pro	Gln	Lys	Ser	Ser	Leu	Glu	Glu	Pro	Asp	Phe	Tyr	Lys	Thr	Lys
			180					185					190		
Ile	Lys	Leu	Cys	Ile	Leu	Leu	His	Ala	Phe	Arg	Ile	Arg	Ala	Val	Thr
	195						200					205			
Ile	Asn	Arg	Met	Met	Ser	Tyr	Leu	Asn	Ser	Ser					
	210					215									

<210> 30

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Sequence

<400> 30

Met	Cys	Pro	Ala	Arg	Ser	Leu	Leu	Leu	Val	Ala	Thr	Leu	Val	Leu	Leu
1				5					10					15	
Asp	His	Leu	Ser	Leu	Ala	Arg	Asn	Leu	Pro	Val	Ala	Thr	Pro	Gly	Pro
		20						25					30		
Gly	Met	Phe	Pro	Cys	Leu	His	His	Ser	Gln	Asn	Leu	Leu	Arg	Ala	Val
		35					40					45			
Ser	Asn	Met	Leu	Gln	Lys	Ala	Arg	Gln	Thr	Leu	Glu	Phe	Tyr	Ser	Cys
	50					55					60				
Thr	Ser	Glu	Glu	Ile	Asp	His	Glu	Asp	Ile	Thr	Lys	Asp	Lys	Thr	Ser
65					70					75					80
Thr	Val	Glu	Ala	Cys	Leu	Pro	Leu	Glu	Leu	Ile	Lys	Asn	Glu	Ser	Cys
				85					90					95	
Leu	Asn	Ser	Arg	Glu	Thr	Ser	Phe	Ile	Thr	Asn	Gly	Ser	Cys	Leu	Ala
			100					105					110		
Ser	Arg	Lys	Thr	Ser	Phe	Met	Thr	Thr	Leu	Cys	Leu	Ser	Ser	Ile	Tyr
		115					120					125			
Glu	Asp	Leu	Lys	Met	Tyr	Gln	Val	Glu	Phe	Lys	Ala	Met	Asn	Ala	Lys
	130					135					140				
Leu	Leu	Met	Asp	Pro	Lys	Arg	Gln	Ile	Phe	Leu	Asp	Gln	Asn	Met	Leu
145					150					155					160
Ala	Ala	Ile	Ala	Glu	Leu	Met	Gln	Ala	Leu	Asn	Val	Asn	Ser	Glu	Thr
				165					170					175	

Ala	Pro	Gln	Lys	Ser	Ser	Leu	Glu	Glu	Pro	Asp	Phe	Tyr	Lys	Thr	Lys
			180					185					190		
Ile	Lys	Leu	Cys	Ile	Leu	Leu	His	Ala	Phe	Arg	Ile	Arg	Ala	Val	Thr
		195					200					205			
Ile	Asn	Arg	Met	Met	Ser	Tyr	Leu	Asn	Ser	Ser					
	210						215								

<210> 31
 <211> 219
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Sequence

<400> 31															
Met	Cys	Pro	Ala	Arg	Ser	Leu	Leu	Leu	Val	Ala	Thr	Leu	Val	Leu	Leu
1				5					10					15	
Asp	His	Leu	Ser	Leu	Ala	Arg	Asn	Leu	Pro	Val	Ala	Thr	Pro	Asp	Pro
			20					25					30		
Gly	Met	Phe	Pro	Cys	Leu	His	His	Ser	Gln	Asn	Leu	Leu	Arg	Ala	Val
		35					40					45			
Ser	Asn	Met	Leu	Gln	Lys	Ala	Arg	Gln	Thr	Leu	Glu	Phe	Tyr	Ser	Cys
	50					55					60				
Thr	Ser	Glu	Glu	Ile	Asp	His	Glu	Asp	Ile	Thr	Lys	Asp	Lys	Thr	Ser
65					70					75					80
Thr	Val	Glu	Ala	Cys	Leu	Pro	Leu	Glu	Leu	Ala	Thr	Asn	Glu	Ser	Cys
				85					90					95	
Leu	Ala	Ser	Arg	Gly	Ile	Ser	Leu	Ile	Thr	Asn	Gly	Ser	Cys	Leu	Ala
			100					105					110		
Ser	Arg	Lys	Thr	Ser	Phe	Met	Thr	Thr	Leu	Cys	Leu	Gly	Ser	Ile	Tyr
		115					120					125			
Glu	Asp	Leu	Lys	Met	Tyr	Gln	Val	Glu	Phe	Lys	Thr	Met	Asn	Ala	Lys
	130					135					140				
Leu	Leu	Met	Asn	Pro	Lys	Arg	Gln	Ile	Phe	Leu	Asp	Gln	Asn	Met	Leu
145					150					155					160
Thr	Ala	Ile	Asp	Glu	Leu	Leu	Gln	Ala	Leu	Asn	Phe	Asn	Ser	Glu	Thr
				165					170					175	
Val	Pro	Gln	Lys	Ser	Ser	Leu	Glu	Glu	Pro	Asp	Phe	Tyr	Lys	Thr	Lys
			180					185					190		
Ile	Lys	Leu	Cys	Ile	Leu	Leu	His	Ala	Phe	Arg	Ile	Arg	Ala	Val	Thr
		195					200					205			
Ile	Asn	Arg	Met	Met	Ser	Tyr	Leu	Asn	Ser	Ser					
	210						215								

<210> 32
 <211> 219
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 32															
Met	Cys	Pro	Pro	Arg	Gly	Leu	Leu	Leu	Val	Ala	Thr	Leu	Val	Leu	Leu
1				5					10					15	
Asp	His	Leu	Ser	Leu	Ala	Arg	Asn	Leu	Pro	Val	Ala	Thr	Pro	Gly	Pro
			20					25					30		
Gly	Met	Phe	Pro	Cys	Leu	His	His	Ser	Gln	Asn	Leu	Leu	Arg	Ala	Val

<210> 34
 <211> 219
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Sequence

<400> 34
 Met Cys Pro Ala Arg Ser Leu Leu Leu Val Ala Thr Leu Val Leu Leu
 1 5 10 15
 Asp His Leu Ser Leu Ala Arg Asn Leu Pro Val Ala Thr Pro Asp Pro
 20 25 30
 Gly Met Phe Pro Cys Leu His His Ser Gln Asn Leu Leu Arg Ala Val
 35 40 45
 Ser Asn Thr Leu Gln Lys Ala Lys Gln Thr Leu Glu Phe Tyr Pro Cys
 50 55 60
 Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser
 65 70 75 80
 Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Ala Thr Asn Glu Ser Cys
 85 90 95
 Leu Ala Ser Arg Gly Ile Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala
 100 105 110
 Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr
 115 120 125
 Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala Met Asn Ala Lys
 130 135 140
 Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu
 145 150 155 160
 Ala Ala Ile Ala Glu Leu Met Gln Ala Leu Asn Val Asn Ser Glu Thr
 165 170 175
 Ala Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys
 180 185 190
 Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val Thr
 195 200 205
 Ile Asp Arg Met Met Ser Tyr Leu Asn Ser Ser
 210 215

<210> 35
 <211> 219
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Sequence

<400> 35
 Met Cys Pro Pro Arg Gly Leu Leu Leu Val Ala Thr Leu Val Leu Leu
 1 5 10 15
 Asp His Leu Ser Leu Ala Arg Asn Leu Pro Val Ala Thr Pro Gly Pro
 20 25 30
 Gly Met Phe Pro Cys Leu His His Ser Gln Asn Leu Leu Arg Ala Val
 35 40 45
 Ser Asn Met Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys
 50 55 60
 Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser
 65 70 75 80
 Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Ile Lys Asn Glu Ser Cys

				85					90				95			
Leu	Asn	Ser	Arg	Glu	Thr	Ser	Phe	Ile	Thr	Asn	Gly	Ser	Cys	Leu	Ala	
			100					105					110			
Ser	Arg	Lys	Thr	Ser	Phe	Met	Thr	Thr	Leu	Cys	Leu	Ser	Ser	Ile	Tyr	
		115					120					125				
Glu	Asp	Leu	Lys	Met	Tyr	Gln	Val	Glu	Phe	Lys	Thr	Met	Asn	Ala	Lys	
	130					135					140					
Leu	Leu	Met	Asn	Pro	Lys	Arg	Gln	Ile	Phe	Leu	Asp	Gln	Asn	Met	Leu	
145					150					155					160	
Thr	Ala	Ile	Asp	Glu	Leu	Leu	Gln	Ala	Leu	Asn	Phe	Asn	Ser	Glu	Thr	
			165						170					175		
Val	Pro	Gln	Lys	Ser	Ser	Leu	Glu	Glu	Pro	Asp	Phe	Tyr	Lys	Thr	Lys	
		180					185					190				
Ile	Lys	Leu	Cys	Ile	Leu	Leu	His	Ala	Phe	Arg	Ile	Arg	Ala	Val	Thr	
	195					200					205					
Ile	Asn	Arg	Met	Met	Ser	Tyr	Leu	Asn	Ser	Ser						
	210					215										

<210> 36
 <211> 219
 <212> PRT
 <213> Homo sapiens

<400> 36																
Met	Cys	Pro	Ala	Arg	Ser	Leu	Leu	Leu	Val	Ala	Thr	Leu	Val	Leu	Leu	
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Asp	His	Leu	Ser	Leu	Ala	Arg	Asn	Leu	Pro	Val	Ala	Thr	Pro	Asp	Pro	
		20					25						30			
Gly	Met	Phe	Pro	Cys	Leu	His	His	Ser	Gln	Asn	Leu	Leu	Arg	Ala	Val	
	35					40					45					
Ser	Asn	Met	Leu	Gln	Lys	Ala	Arg	Gln	Thr	Leu	Glu	Phe	Tyr	Pro	Cys	
	50				55					60						
Thr	Ser	Glu	Glu	Ile	Asp	His	Glu	Asp	Ile	Thr	Lys	Asp	Lys	Thr	Ser	
65				70					75					80		
Thr	Val	Glu	Ala	Cys	Leu	Pro	Leu	Glu	Leu	Thr	Lys	Asn	Glu	Ser	Cys	
			85					90					95			
Leu	Asn	Ser	Arg	Glu	Thr	Ser	Phe	Ile	Thr	Asn	Gly	Ser	Cys	Leu	Ala	
		100					105						110			
Ser	Arg	Lys	Thr	Ser	Phe	Met	Met	Ala	Leu	Cys	Leu	Ser	Ser	Ile	Tyr	
	115					120					125					
Glu	Asp	Leu	Lys	Met	Tyr	Gln	Val	Glu	Phe	Lys	Thr	Met	Asn	Ala	Lys	
	130					135					140					
Leu	Leu	Met	Asp	Pro	Lys	Arg	Gln	Ile	Phe	Leu	Asp	Gln	Asn	Met	Leu	
145				150						155					160	
Ala	Val	Ile	Asp	Glu	Leu	Met	Gln	Ala	Leu	Asn	Phe	Asn	Ser	Glu	Thr	
			165						170					175		
Val	Pro	Gln	Lys	Ser	Ser	Leu	Glu	Glu	Pro	Asp	Phe	Tyr	Lys	Thr	Lys	
		180					185					190				
Ile	Lys	Leu	Cys	Ile	Leu	Leu	His	Ala	Phe	Arg	Ile	Arg	Ala	Val	Thr	
	195					200					205					
Ile	Asp	Arg	Val	Thr	Ser	Tyr	Leu	Asn	Ala	Ser						
	210					215										

<210> 37
 <211> 987
 <212> DNA
 <213> Homo sapiens

<400> 37

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gcccctggag	aaatggtggt	cctcacctgt	gacacccctg	aagaagatgg	tatcacctgg	180
accttggacc	agagcagtga	ggtcttaggc	tctggcaaaa	ccctgaccat	ccaagtcaaa	240
gagtttggag	atgctggcca	gtacacctgt	cacaaaggag	gcgagggttct	aagccattcg	300
ctcctgctgc	ttcacaaaaa	ggaagatgga	atgttggtcca	ctgatatttt	aaaggaccag	360
aaagaaccca	aaaataagac	ctttctaaga	tgcgaggcca	agaattattc	tggacgtttc	420
acctgctggt	ggctgacgac	aatcagtact	gatttgacat	tcagtgtcaa	aagcagcaga	480
ggctcttctg	acccccaaag	ggtgacgtgc	ggagctgcta	cactctctgc	agagagagtc	540
agaggggaca	acaaggagta	tgagtactca	gtggtagtgc	aggaggacag	tgcttgccca	600
gctgctgagg	agagtctgcc	cattgagggtc	atgggtggatg	ccgttcacaa	gctcaagtat	660
gaaaactaca	ccagcagctt	cttcatcagg	gacatcatca	aacctgaccc	acccaagaac	720
ttgcagctga	agccattaaa	gaattctcgg	cagggtggagg	tcagctggga	gtaccctgac	780
acctggagta	ctccacattc	ctacttctcc	ctgacattct	gcgttcaggt	ccagggcaag	840
agcaagagag	aaaagaaaga	tagagtcttc	acggacaaga	cctcagccac	ggtcattctgc	900
cgcaaaaatg	ccagcattag	cgtgcggggc	caggaccgct	actatagctc	atcttggagc	960
gaatgggcat	ctgtgccttg	cagttag				987

<210> 38

<211> 660

<212> DNA

<213> Homo sapiens

<400> 38

atgtgtccag	cgcgcagcct	cctccttgtg	gctaccctgg	tcctcctgga	ccacctcagt	60
ttggccagaa	acctccccgt	ggccactcca	gacccaggaa	tgttcccatg	ccttcaccac	120
tcccaaaaacc	tgctgagggc	cgtcagcaac	atgctccaga	aggccagaca	aactctagaa	180
ttttaccctt	gcacttctga	agagattgat	catgaagata	tcacaaaaga	taaaaccagc	240
acagtggagg	cctgtttacc	attggaatta	accaagaatg	agagttgcct	aaattccaga	300
gagacctctt	tcataactaa	tgggagttgc	ctggcctcca	gaaagacctc	ttttatgatg	360
gccctgtgcc	ttagtagtat	ttatgaagac	ttgaagatgt	accagggtgga	gttcaagacc	420
atgaatgcaa	agcttctgat	ggatcctaag	aggcagatct	ttctagatca	aaacatgctg	480
gcagttattg	atgagctgat	gcaggccctg	aatttcaaca	gtgagactgt	gccacaaaaa	540
tcctcccttg	aagaaccgga	tttttataaa	actaaaatca	agctctgcat	acttcttcat	600
gctttcagaa	ttcgggcagt	gactattgac	agagtgcaga	gctatctgaa	tgcttcctaa	660

<210> 39

<211> 328

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Sequence

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<223> C or H

<221> VARIANT

<222> (3)...(3)

<223> H or P

<221> VARIANT

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<223> I or V

<221> VARIANT

<222> (15)...(15)

<223> F or L

<221> VARIANT
<222> (21)...(21)
<223> V or M

<221> VARIANT
<222> (27)...(27)
<223> K or E

<221> VARIANT
<222> (29)...(29)
<223> D or N

<221> VARIANT
<222> (40)...(40)
<223> D or N

<221> VARIANT
<222> (45)...(45)
<223> M or T

<221> VARIANT
<222> (49)...(49)
<223> T or A

<221> VARIANT
<222> (62)...(62)
<223> S

<221> VARIANT
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<223> E or G

<221> VARIANT
<222> (71)...(71)
<223> T

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<223> H

<221> VARIANT
<222> (91)...(91)
<223> H or R

<221> VARIANT
<222> (95)...(95)
<223> E, A, K, or T

<221> VARIANT
<222> (96)...(96)
<223> V or A

<221> VARIANT
<222> (99)...(99)
<223> R or Q

<221> VARIANT
<222> (122)...(122)
<223> E or K

<221> VARIANT

<222> (125)...(125)
<223> N or A

<221> VARIANT
<222> (127)...(127)
<223> S or I

<221> VARIANT
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<221> VARIANT
<222> (135)...(135)
<223> N or D

<221> VARIANT
<222> (139)...(139)
<223> R or H

<221> VARIANT
<222> (147)...(147)
<223> T or A

<221> VARIANT
<222> (153)...(153)
<223> T or K

<221> VARIANT
<222> (155)...(155)
<223> S or T

<221> VARIANT
<222> (163)...(163)
<223> S or T

<221> VARIANT
<222> (166)...(166)
<223> Q, R, or H

<221> VARIANT
<222> (172)...(172)
<223> A or T

<221> VARIANT
<222> (173)...(173)
<223> A or V

<221> VARIANT
<222> (174)...(174)
<223> T or L

<221> VARIANT
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<223> A or E

<221> VARIANT
<222> (178)...(178)
<223> E or D

<221> VARIANT
<222> (179)...(179)

<223> R, L, or K

<221> VARIANT

<222> (180)...(180)

<223> V or G

<221> VARIANT

<222> (181)...(184)

<223> deleted, or replaced with S-(L or M)-(E or D)-H-R

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<223> E

<221> VARIANT

<222> (186)...(186)

<223> Y

<221> VARIANT

<222> (187)...(187)

<223> K or N

<221> VARIANT

<222> (188)...(188)

<223> K

<221> VARIANT

<222> (190)...(190)

<223> R or T

<221> VARIANT

<222> (196)...(196)

<223> G

<221> VARIANT

<222> (201)...(201)

<223> A or S

<221> VARIANT

<222> (211)...(211)

<223> V

<221> VARIANT

<222> (212)...(212)

<223> V or L

<221> VARIANT

<222> (213)...(213)

<223> D or E

<221> VARIANT

<222> (215)...(215)

<223> V or I

<221> VARIANT

<222> (226)...(226)

<223> S or R

<221> VARIANT

<222> (244)...(244)

<223> K or R

<221> VARIANT
<222> (251)...(251)
<223> Q or H

<221> VARIANT
<222> (254)...(254)
<223> V or I

<221> VARIANT
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<223> S or N

<221> VARIANT
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<223> E or G

<221> VARIANT
<222> (264)...(264)
<223> T or A

<221> VARIANT
<222> (274)...(274)
<223> C or G

<221> VARIANT
<222> (275)...(275)
<223> V or I

<221> VARIANT
<222> (280)...(280)
<223> K or R

<221> VARIANT
<222> (281)...(281)
<223> S or N

<221> VARIANT
<222> (285)...(285)
<223> K or D

<221> VARIANT
<222> (286)...(286)
<223> K or R

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<222> (287)...(287)
<223> D or deleted

<221> VARIANT
<222> (288)...(288)
<223> R or deleted

<221> VARIANT
<222> (289)...(289)
<223> I or L

<221> VARIANT
<222> (291)...(291)
<223> T or M

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<223> K or Q

<221> VARIANT
<222> (297)...(297)
<223> T or K

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<222> (299)...(299)
<223> I, T, or V

<221> VARIANT
<222> (301)...(301)
<223> R or H

<221> VARIANT
<222> (303)...(303)
<223> N or D

<221> VARIANT
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<223> Q

<221> VARIANT
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<223> R

<221> VARIANT
<222> (315)...(315)
<223> Y or H

<221> VARIANT
<222> (318)...(318)
<223> S or F

<221> VARIANT
<222> (321)...(321)
<223> E or D

<221> VARIANT
<222> (326)...(326)
<223> P or S

<221> VARIANT
<222> (327)...(327)
<223> C or L

<221> VARIANT
<222> (328)...(328)
<223> S, G, or Q

<400> 39

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Ala	Ser	Pro	Leu	Xaa	Ala	Ile	Trp	Glu	Leu	Xaa	Lys	Xaa	Val	Tyr	Val
			20					25					30		
Val	Glu	Leu	Asp	Trp	Tyr	Pro	Xaa	Ala	Pro	Gly	Glu	Xaa	Val	Val	Leu
		35					40					45			
Xaa	Cys	Asp	Thr	Pro	Glu	Glu	Asp	Gly	Ile	Thr	Trp	Thr	Xaa	Asp	Gln
	50					55					60				
Ser	Ser	Xaa	Val	Leu	Gly	Xaa	Gly	Lys	Thr	Leu	Thr	Ile	Xaa	Val	Lys
65					70					75					80
Glu	Phe	Gly	Asp	Ala	Gly	Gln	Tyr	Thr	Cys	Xaa	Lys	Gly	Gly	Xaa	Xaa
				85					90					95	
Leu	Ser	Xaa	Ser	Leu	Leu	Leu	Leu	His	Lys	Lys	Glu	Asp	Gly	Ile	Trp
			100					105					110		
Ser	Thr	Asp	Ile	Leu	Lys	Asp	Gln	Lys	Xaa	Pro	Lys	Xaa	Lys	Xaa	Phe
		115					120					125			
Leu	Xaa	Cys	Glu	Ala	Lys	Xaa	Tyr	Ser	Gly	Xaa	Phe	Thr	Cys	Trp	Trp
	130					135					140				
Leu	Thr	Xaa	Ile	Ser	Thr	Asp	Leu	Xaa	Phe	Xaa	Val	Lys	Ser	Ser	Arg
145					150				155						160
Gly	Ser	Xaa	Asp	Pro	Xaa	Gly	Val	Thr	Cys	Gly	Xaa	Xaa	Xaa	Leu	Ser
			165						170					175	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Tyr	Xaa	Val	Glu
			180					185					190		
Cys	Gln	Glu	Xaa	Ser	Ala	Cys	Pro	Xaa	Ala	Glu	Glu	Ser	Leu	Pro	Ile
		195					200					205			
Glu	Val	Xaa	Xaa	Xaa	Ala	Xaa	His	Lys	Leu	Lys	Tyr	Glu	Asn	Tyr	Thr
	210					215					220				
Ser	Xaa	Phe	Phe	Ile	Arg	Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Lys	Asn
225				230					235					240	
Leu	Gln	Leu	Xaa	Pro	Leu	Lys	Asn	Ser	Arg	Xaa	Val	Glu	Xaa	Xaa	Trp
			245					250					255		
Xaa	Tyr	Pro	Asp	Thr	Trp	Ser	Xaa	Pro	His	Ser	Tyr	Phe	Ser	Leu	Thr
		260					265					270			
Phe	Xaa	Xaa	Gln	Val	Gln	Gly	Xaa	Xaa	Lys	Arg	Glu	Xaa	Xaa	Xaa	Xaa
		275					280					285			
Xaa	Phe	Xaa	Asp	Xaa	Thr	Ser	Ala	Xaa	Val	Xaa	Cys	Xaa	Lys	Xaa	Ala
	290					295					300				
Xaa	Ile	Xaa	Val	Xaa	Ala	Xaa	Asp	Arg	Tyr	Xaa	Ser	Ser	Xaa	Trp	Ser
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 Gly Xaa Xaa Xaa Cys Leu Xaa Xaa Ser Gln Asn Leu Leu Xaa Ala Xaa
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 Thr Ser Glu Glu Xaa Asp His Glu Asp Ile Thr Xaa Asp Lys Thr Ser
 65 70 75 80
 Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Xaa Xaa Asn Glu Ser Cys
 85 90 95
 Leu Xaa Ser Arg Xaa Xaa Ser Xaa Ile Thr Asn Gly Ser Cys Leu Ala
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 Ser Arg Lys Thr Ser Phe Met Xaa Xaa Leu Cys Xaa Xaa Ser Ile Tyr
 115 120 125
 Glu Asp Leu Lys Met Tyr Gln Xaa Glu Phe Lys Xaa Met Asn Ala Lys
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